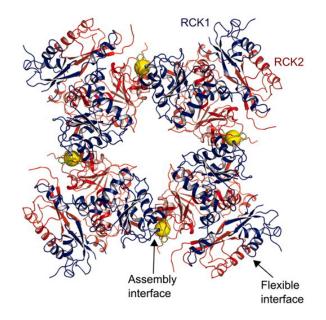
Flexible Access and Highly Automated Beamline for Macromolecular Crystallography (AMX)

AMX at NSLS-II

- Will provide structural biologists with ready access to an advanced facility for precise structure determinations at unprecedented rates
- Will optimally exploit unique source characteristics and deliver a very high flux in a suitably small focused beam
- Will be highly automated to support remote access and extensive experimental studies

Examples of Science Areas & Impact

- STRUCTURAL BIOLOGY: Atomic structures of large protein and nucleic acid complexes, including membrane proteins, are prerequisites to gaining insights into their function, and interactions, thus creating molecular movies
- BIOCHEMISTRY: Structural analysis of all intermediates in entire enzymatic cycles and pathways will expand our understanding of cellular and microbiological processes
- PHYSIOLOGY AND MEDICINE: Crystallographic studies of the interactions of drugs with their targets are essential in the development of improved and new pharmacologically effective compounds



Ribbon diagram of the gating ring of the human BK channel Ca-activation apparatus. This channel encodes negative feedback regulation of membrane voltage and Ca-signaling, which plays a central role in numerous physiological processes.

P.Yuan, MD Leonetti, AR Pico, Y Hsiung and Roderick MacKinnon, Science 329, 182-6 (2010).

Beamline Capabilities

TECHNIQUE: macromolecular crystallography

Source: canted U20 In-vacuum undulator

ENERGY RANGE / RESOLUTION: 5-20 keV; $\Delta E/E$

~5x10⁻⁴

SPATIAL RESOLUTION: beam size from 6x5 to 300

 μ m² (diffraction resolution to < 1 Å)



